

GenCore version 4.5
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OM nucleotide - nucleic search, using sw model

Run on: February 9, 2000, 11:00:06, Search time 5590.77 seconds

Title: US-09-190-246-1
 Perfect score: 1538
 Sequence: 1 tcygcgttcctggcgtac.....tatcagcgcccttcgc 1538
 Scoring table: IDEMTV_NJC
 Searched: 4538634 seqs, 1897931982 residues

Database : EST.*
 Word size : 0

Number of hits that pass the threshold : 907268

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[illegible]

[illegible][illegible]

sun Feb 13 13:44:50 2000

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Oy 1346 TGGCAAAACCCAGAGATGAGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTG 13405
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Oy 13466 AGCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 13525
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Oy 13526 TCGAGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 13585
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RESULT 4
ACB56202/c 757 bp DNA GSS 03-NOV-1999
LOCUS nebb001P05f, genomic survey sequence.
DEFINITION A BAC End Sequencing Framework to Sequence the Rice Genome
ACCESSION ACB56202.1 GI:4206659
KEYWORDS GSS
SOURCE Oriza sativa.
ORGANISM Oriza sativa.
REFERENCE 1. Wang, H.A. and Dean, H.A.
AUTHORS A BAC End Sequencing Framework to Sequence the Rice Genome
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL (J. Heredity)
COMMENT Contact: Ming RA
Clemson University Genomics Institute
Clemson University
Clemson, SC 29634, USA
Tel: 864 656 7188
Fax: 864 656 4293
E-mail: ming.ra@clmson.edu
Seq primer: TATGAGTACTACTAGAG
Class: BAC ends
High quality sequence start: 29
High quality sequence stop: 232
High quality sequence length: 232
Location/Qualifiers
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location=Oriza sativa
strain=Japanica
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FEATURES
source

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/clone.lib="nebb001P05f"
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/name=vector: pacBACindigo: site:1: Ecoli; Site:2: Ecoli;
Rice is the most important food crop in the world. It is grown in the world's tropics and subtropics, rely
on rice as their primary source of carbohydrate, with a
Monocotyledonous rice as a staple food. Map (Arumuganathan and
Baril, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic mapping and genome sequencing of rice,
we have constructed a BAC library from Oriza sativa, the
Nipponbare variety, using EcoRI and BamHI restriction
enzymes. The library contains approximately 150,000 clones
of 121 kb providing approximately 15 haploid genome
equivalents. The deep coverage allows the identification
of particular sequences. The library contains approximately
18,432 clones (doubly spotted), represent the whole library for colony
screening and can be requested from the University
of California, Davis (http://www.genome.ucdavis.edu).
BAC/180 C 176 9 185 T 10 others
BASE COUNT 204 A 180 C 176 9 185 T 10 others
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Matches 705; Conservative 0; Mismatches 51
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EXHIBIT

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us-09-190-246-1.rst

Sun Feb 13 13:44:50 2000

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RESULTS
US Patent No. 5,263A-1
Sequence 1, Application US/08801263A
Patent No. 5811407
GENE NAME: HEMOPHILIN.
APPLICANT: Johnston, Robert E.
APPLICANT: Davis, Nancy L. A.
APPLICANT INVENTOR: System for the In Vivo Delivery and Expression of Heterologous Genes in the Bone Marrow OF MAMMARY GLANDS AND BLOOD VESSELS
TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow NUMBER OF SEQUENCES: 2
COMMENTS: See Sequence 2
ADDRESSSEE: Ball Seltzer Park & Gibson, P.A.
STREET: 1211 East Morehead Street
CITY: Charlotte, N.C. 28204
STATE: NC 28204
COUNTRY: USA
ZIP: 28234
COMPUTER: IBM compatible PC
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: DOS
CURRENT FILE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,263A
PUBLICATION NUMBER: 11997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Marybeth Smith
REFERENCE NUMBER: 31,665
TRANSMISSION NUMBER 31: 5470-147
TELECOMMUNICATION INFORMATION:
FAX NUMBER: 919-881-3175
TELEPHONE: 919-881-3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SOURCE: CHANGING CELL LINE
TYPE: nucleic acid
STRANDEDNESS: double
FEATURES:
MOLECULE TYPE: cDNA
NAME/KEY: COS
FEATURES:
NAME/REV: COS
NUMBER: 1
FEATURES: 68..7559
FEATURES: 7686..11342
US-08-801-263A-1

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[illegible]

US-95-102-248-1
Sequence No. 6010248
Publication US/9310248
GENERAL INFORMATION:
INVENTOR: DEVLIN, ROBERT E.
APPLICANT: DEVLIN, NANCY L.
ATTORNEY: SLIMMON, SYSTEM FOR THE IN VIVO DELIVERY AND
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS GENES IN THE BONE MARROW
OF MAMMALS
CORRESPONDENCE ADDRESS:
ADDRESSER: BALL SALTZER FAY & GIBSON, P.A.
STREET:

STATE: No. 6008035th Carolina
COUNTRY: USA
CITY: Charlotte
CONTRACT NO.: 6633A
CONTRACTOR: IBM
COMPUTER READABLE FORM:
MEDIUM TYPE: 8 INCH FLOPPY
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0. Version #1.30
COMPILED BY: IBM
APPLICATION NUMBER: US/09/102,248
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US 08/801,263
FILING DATE: 19-FEB-1997
AUTHOR/CONTROLLER:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665 90-147

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[illegible]

[illegible]

RESULT 12
 US-09-102-248-4
 Sequence 4, Priority 1
 GENERAL INFORMATION:
 APPLICANT: Johnston, Robert E.
 APPLICANT: Davis, Nancy L.
 APPLICANT: Williams, A.
 TITLE OF INVENTION: System for the In Vivo Delivery and
 Titration of Heterologous Genes
 CORRESPONDENCE ADDRESS: 2
 ADDRESSEE: Bell Seitzer Park & Gibson, P.A.
 CITY: Chicago, Illinois
 STATE: No. 6060835th State
 COUNTRY: USA
 EXPIRATION DATE: 03/22/94
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 FILED IN: IBM PC compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 COUNTRY OF ORIGIN: USA
 APPLICATION NUMBER: 05/09/102.248
 FILING DATE:
 PRIORITY CLASSIFICATION:
 APPLICATION NUMBER: US 08/601.263
 FILING DATE: 13-FEB-1997
 ANOTHER NUMBER:
 NAME: SUBVISOR
 REGISTRATION INFORMATION: 6
 REGISTRATION NUMBER: 5470-147
 TELECOMMUNICATIONS SECTION:
 TELEPHONE: 915-420-2200

TELEFAX: 919-881-9175
INFORMATION FOR SED IN NO. 4;
SEQUENCE CHARACTERISTICS:
LENGTH: 1117 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
J5-09-102-248-4

[illegible]

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Copied from 09549937 on 04/17/2006

[illegible]

[illegible][illegible]

[illegible]

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 Db 2282 TATTAAG 2341
 Qy 4828 taataag 2401
 Db 2342 TATTAAG 2401
 Qy 4888 gaaatgt 2461
 Db 2402 CTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2461
 Qy 5008 gggag 5067
 Db 2462 GGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2521
 Qy 5068 gggag 2581
 Db 2522 GGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT

[illegible]

KN	CwVlnA-G8M; vector: plasmid Vlnno; db.
CC	Synthetic.
FN	W9524485-A2.
PP	15 MAR-1995.
PR	03-MAR-1995.
PA	U03633.
PR	07-MAR-1994; U5-207526.
PA	(MERI) MERCK & CO INC.
PT	WPI-32477 MC. Silver JW;
PT	New poly-clonetic expression construct - for producing antigens and
PT	immuno-stimulatory gene products useful as vaccines against e.g.
PT	Chlamydia, etc
PT	Immunostim., etc 9g, 176pp; English.
CC	Vector Vlnno (W0114); val.
CC	replacement of the amp ^r -resistance gene by
CC	the resistance gene. The vector also contains a CwVlnA-G8M terminator
CC	sequence (nt 213-217).
CC	genes. Insertion of HIV into the vector allows
CC	large-scale production of polypeptide vaccine in bacterial host
CC	Scale-up: 4664 ml; 2000

[illegible]

Db	2538	TAACTCCAGGAGAGACATCTGATGCAAGGCGACGACGCTGAAAAGCG	2597
Oy	13273	CGGTCTGCGGTGTTTTCCTCCTAGGCTCGCCCTCGGAGATCGAATCAACGCG	13393
Db	2598	CGGCTTGTCTGGCGTTTTCATATAGCTCTGCGCCCTCGAGCATCATCAAAATTCGAG	2657
Oy	13333	CTCATATCTAGAGTGGCGACACACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	13392
Db	2658	CTCATATCTAGAGTGGCGACACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	2717
Oy	13393	CTCATATCTAGAGTGGCGACACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	13432
Db	2718	AAGCTCTCGTCTGCTTCTCCAGCTCGCGCTGCTACGAGATCAAGCGCTTCCCTCCG	2777
Oy	13453	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	13512
Db	2777	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	2837
Oy	13513	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	13572
Db	2838	TGAGTGGTCTGCTCTCAAGCTGGCGCTGTGACAGACCGCTCGATCGACCGAGCT	2897
Oy	13573	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	13632
Db	2897	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	2957
Oy	13633	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	13692
Db	2958	CGACGACGCCATCGTGTACAGAGATTAGAGACGAGATTTTGGATATTCGCGTCT	3017
Oy	13693	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	13752
Db	3018	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	3077
Oy	13753	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	13812
Db	3078	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	3137
Oy	13813	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	13872
Db	3138	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	3197
Oy	13873	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	13932
Db	3198	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	3257
Oy	13933	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	13992
Db	3258	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	3317
Oy	13993	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	14052
Db	3318	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	3377
Oy	14053	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	14112
Db	3378	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	14172
Oy	14113	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	14172
Db	3493	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	3497
Oy	14173	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	14232
Db	3498	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	3557
Oy	14233	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	14292
Db	3558	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	3617
Oy	14293	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	14352
Db	3618	CTCATATCTAGAGTGGCGACACACAGAGCTATAAGATCAAGCGCTTCCCTCCG	3677

QY 15432 aggggtctccgcgaacttcccgcgagaaatcagaacacccaaccgcccaaacacacatttat 15431
DB 4759 AGGGGTCTCCGCGACATTTCCCAGCAAAATGCCACTTCGAAGTCTTAGAACACCATATTAT 4917

QY 15492 catgatcatcatttttcataatcatttgcagtcttgatcgaggctggctgttc 1538
DB 4818 CATGACATTAACCCTAATAAAAAATGAGCCTATGCAGAGGGCCCCCTTCCTC 1864

BESTFIT 4
ID VJ1337 standard; DNA; 4864 BP.
AC 21-JUN-1998 (first entry)
DE Viljmo sequence used for construction of synthetic HIV new RNA
KW Viljmo; HIV vaccine; codon usage optimized against AIDS patients; response;
NM HIV protein; recombinant; ds.
OS Synthetic O.E.
PN W6974837.9.AZ
PP 17-JUN-1997; U10517.
PR 16-JUL-1996; GB-011943
PR 16-JUN-1996; US-021066
PR 16-JUN-1996; US-021066
PR 16-JUN-1996; GB-011942
PA (MERT) MERCK & CO INC.
PI 98-02425/06.
PT cell - genome rev-independent expression of HIV genes
PS Example 4; Pages 73-76; 113pp; English.
SC This Viljmo sequence is unique. The synthetic RNA sequence encodes HIV.
CC noncodon or a fragment and has codons optimised for expression in a
CC non-homologous host. The synthetic DNA sequences anti-HIV neutralising
CC production of specific T-cell immune responses or protective immune
CC responses in vertebrates, specifically as HIV vaccines. Optimisation
CC of codons results in increased uptake into lymphocyte cytosolic and helper
CC DNA binding and effector functions such as stimulate cytokine secretion specific
CC to HIV antigens. Cross-strain protection is achieved by inclusion of
CC adjuvant and the synthesis proportion of codons rarely used in mammals. So
CC optimisation will allow this gene to be expressed efficiently in mammalian
CC of rev. The DNA sequences are more generally applicable to other systems
CC other pathogens e.g. AIDS A; 1226 C; 1158 G; 1241 T;
CC sequence 4894 BP.

Query Match
Local Similarity 99.7%; Pred. No. 0;
Matches 2978; Conservative 8; Mismatches 1; Gaps 1;

QY 12553 aaactcgtctgctcgaatgcgcacctggtgccccctccctccctccttc 12612
DB 1878 AGATCTGCTTGCTCTGTATGTTGCCMGCTCTGTGTTCCTCCCTCCCGCTCTCC 1937

QY 12613 tgcacotcgaagatgcacotccctccctcctctctaataaagagaatatgtag 12672
DB 1938 ATGCATCTGAGATGGCATCCCTCCCTCTCTCTTCAATAGAAGGAANTTCGATNG 1997

QY 12673 ttgcactcgtcgtgtctctctctctcctccgtgggggtaaggtcgggcgaagaagaag 12732
DB 1998 CATCTCTGAGTAAAGTGTATTCATCTGGGGGATGGGGTGGCGACACAGCACAGG 2057

QY 12733 gsgaatcgtggaagaacaacacagcgctgctggatcggctggatcttgtggatccag 12792
DB 2058 HGRHTTGGGAAGACACAGAGAGCGGCTTCGTGGGAGTCGGTGGGCTATGATGACCCAG 2117

QY 12793 gtgcataatgtagcccgcttccctccctgggcgaagaagaagapacacccctcttc 12852

[illegible]

[illegible][illegible]

C response (both humoral and cellular) in hosts, human or animal,
C susceptible to Lyme disease (claimed). It can also be used for the
C production of a Borrelia antigen in vitro in eukaryotic cells
C (claimed), and these antigens used as vaccines or immunogenic
C compositions, or to produce monoclonal antibodies. 1457 T:
C Sequence: 5843 bp; 1611 A; 1390 C; 1385 G; 1457 T;

[illegible][illegible]

[illegible]

Oy 5085 cggattcctaataatgatgccttaaggtgaactcaacac-----aaactctg 5145
 Db 2531 cggattcctaataatgatgccttaaggtgaactcaacac-----aaactctg 2590
 Oy 5145 cctgaagatgataataaataataacagagcttgagcgttcctatccgcgcctt 5205
 Db 2531 taccacacacattctacaggtttttctccctccagctgttcacacacacacac 5260
 Oy 5206 gctcgtttgctcagcttgagcttgagctgagcagcagcagctgcaaacacacat 5265
 Db 2651 atgcagacattctgtttgagatggaatattgaacacacacacacacacacacac 5310
 Oy 5266 cctcagcctcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5325
 Db 2711 atctcagcctcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5380
 Oy 5326 aggtctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5385
 Db 2771 atctcagcctcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5445
 Oy 5386 actcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5450
 Db 2831 ctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5490
 Oy 5446 ctctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5505
 Db 2891 cctctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5560
 Oy 5506 gctctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5565
 Db 2951 atctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5610
 Oy 5566 taactctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5625
 Db 3011 aaattttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5680
 Oy 5626 gtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5685
 Db 3071 aaac 5745
 Oy 5686 agagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5750
 Db 3131 agcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5810
 Oy 5746 cctatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5815
 Db 3191 cctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5880
 Oy 5805 tgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5885
 Db 3351 ttgctatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5904
 Oy 5866 cctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5904
 Db 3311 gttttagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5970
 Oy 5905 tgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 5970
 Db 3371 aaac 5984
 Oy 5965 cctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6024
 Db 3431 gttttagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6024
 Oy 6025 gctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6084
 Db 3486 taattctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6084
 Oy 6085 tgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6144
 Db 3548 cctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6144

Oy 6145 cctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6204
 Db 3608 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6204
 Oy 6205 gtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6264
 Db 3658 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6264
 Oy 6265 gtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6324
 Db 3728 cctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6324
 Oy 6325 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6384
 Db 3785 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6384
 Oy 6385 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6444
 Db 3845 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6444
 Oy 6442 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6501
 Db 3905 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6501
 Oy 6502 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6561
 Db 3965 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6561
 Oy 6562 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6621
 Db 4025 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6621
 Oy 6622 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6681
 Db 4085 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6681
 Oy 6682 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6741
 Db 4145 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6741
 Oy 6742 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6801
 Db 4205 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6801
 Oy 6802 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6861
 Db 4265 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6861
 Oy 6862 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6921
 Db 4325 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6921
 Oy 6922 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6981
 Db 4385 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 6981
 Oy 6982 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 7041
 Db 4443 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 7041
 Oy 7043 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 7101
 Db 4505 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 7101
 Oy 7102 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 7158
 Db 4565 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 7158
 Oy 7158 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 7218
 Db 4625 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 7218
 Oy 7219 ctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 7278

[illegible]

7339 gctgcgagaaacatggacatccagatccaaatgctcggtagcgaactgcctgcatc 7398
7340 gctgcgagaaacatggacatccagatccaaatgctcggtagcgaactgcctgcatc 7399
4805 ATTGGGGGAGACATCATGAGCAATATCGCGAAMATATTTTTTTTTTTTTTT 4864
7399 aacacccctccgacagatgctgcctgctgctgcctgcctgcctgcctgcctgc 7458
4865 TAGCCGCTCCGAAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4924
7459 cctcttagctagccacccaatcaaaagcatggtggttgcctatctttccctccaa 7518
4925 CAGATCTACACAGCATACATGCTGAGAGTACAGATATGCTGCTCCACCCCTTCGA 4984
7519 atataccttagatgggtagaagctaaagctgaagctaaagctgaagctgaagctga 7578
4985 GTACAAATCTGAGATGTTTCAGAGGTTTAACTGAGGATGAGGATGAGGATGAG 5044
7579 ggtacctccttggttcctgcgaagctaaatgagctatctagagagaaacatcagatc 7638
5045 TAGCCGCGATTTGCTCCGCGCTTACCTGAGGATGAGGATGAGGATGAGGATGAG 5104
7639 gctgttacc--gaggtgttgctgctgctgctgctgctgctgctgctgctgctgctg 7695
5105 GCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5164
7696 taactatgtaact-- 7713
5165 TAGACATCTGCTTGATCTGCGCATATCTGCTGCACTGAGGAGGATGAGGAGGAG 5224
7714 ttacacatcttgagcctgcgactgcgactgcgactgcgactgcgactgcgactgcg 7773
5225 ACTCTTTTCAGGCTTTTACGAGTATGAGCATCTGAGCACTCAGAGGAGGAGTGTGTGTG 5284
7774 tgccttaacatccctgaaccccgagcgtgcgtgcgactgcgctgcgctgcgctgcgctgc 7833
5285 CAGACCGCTCTCAAGGCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5344
7834 cgcagacatgtagcctctgcagcgcagcctctccacgcagcgcagcgcagcgcagcgc 7888
5345 GCACCGCGCGAG 5404
7888 ----tgatcattgctctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgc 7923
5405 GTCCCTTCACCTCTCTTTGATGGGGTATCTATATCTTGGATCTTGGATCTTGGATCGAG 5464
7924 cgcgcgcgcgaagaacgcagcgtgcgtgccacagagcgcgttgtagaacacagctgccttc 7983
5465 GATGCGCTCTGGCAGCGCGACACACCTCCGACGATACAGCTACGCTACGCTACGCTACG 5524
7984 gaagtttcgcgcgttccttgtagcgcagcgcagctgcagctgcgcgcgcgcgcgcgcgcgc 8043
5525 CTCTTCGATGCTTTTTCGACAGAGGATGAGGAGGTTGAGCGCGAGAGTACCGCGATC 5584
8044 aactcttgaa-- 8054
5585 GGAGCGCTCTCTTGGCTCTTGAACCGCGCGAGAGTGCATCATATATCTCTCCG 5644
8054 ----gaagct-- 8058
5645 ATCAACCGTATCTTTTCACACGACAGCAGACGATAGACGCGAGAGAGAGAGAGAGAG 5704
8059 cctgc 8118
5705 ATTTCTTACACCGCGCTGAGCGTGGTACATATTTTCGCGAGACACACCGCTCTGGAGCT 8176
8119 aacacaaaacaccttaggc 8178
5715 GCNAAAGAGCTCGCTTCGACAGACCGCTCTCAACCGAGAGAGAGAGAGAGAGAGAGAG 5824
8179 ggaagaaatgtagccgcgcaaaatgtagatagagtagagtagagtagagtagagtagagtag 8238
5825 ggaatggaatgtagccgc 8299
8239 ghaatgtagccgc 8299

[illegible]

Db 3251 TTGCAATTAAGTTTTCGGCATGGCTTCACAGCGAGCTTTCTTACAGAGCATCC 3310
 Qy 5866 cctgattatagagaaac-----cactggataaactactcga 5904
 Db 3311 ATTAAGATGTCGCGCGGATGATGACGAGCGGCTAGCTTTTGGAGCAACCGGAC 3770
 Qy 5905 tggaaagttctatggtctaaagtcagcaacagctgcggctgtggagctatgataactc 5964
 Db 3371 AACCGCGAGTATGGGATGATGATGATGATGATGATGATGATGATGATGATGAT 3430
 Qy 5965 cctgaggggctggagctgagctgagctgagctgagctgagctgagctgagctgagct 3430
 Db 3431 GTTCAGCTAGCTGGG-----AAGGCGCAACGATGATGATGATGATGATGATGAT 6024
 Qy 6025 gcttctctgagctgagctgagctgagctgagctgagctgagctgagctgagct 3487
 Db 3488 TATCTGTCGACGATTAACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 6084
 Qy 6085 tggctgctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 6144
 Db 3548 CAGTATGAG 3607
 Qy 6145 ccaagctgctgctggagctgagctgagctgagctgagctgagctgagctgagctgagct 6204
 Db 3608 CTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3667
 Qy 6205 gtacagctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 6274
 Db 3668 CGCCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 3737
 Qy 6267 tggctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 6324
 Db 3728 GAGGCG-----ACGTGAGAGCTGGCTGATGATGATGATGATGATGATGATGATGAT 3784
 Qy 6325 ctacagagctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 3844
 Db 3785 CTTCAGCGATGCGAG 3844
 Qy 6385 atcgctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 6441
 Db 3845 TTGCTGCTTACCGAG 3904
 Qy 6442 cgaagctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 6501
 Db 3905 TAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3964
 Qy 6502 ttgctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 6558
 Db 3965 TTGCTGCTTACCGAG 6594
 Qy 6559 gagaactctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 6618
 Db 4025 AGCGGATTTACCGCGCGCTGATGATGATGATGATGATGATGATGATGATGATGAT 6678
 Qy 6619 catgagctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 6738
 Db 4082 AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4141
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 Db 4142 TCAG 4201
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 Db 4322 GAGGAG 4381
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Best Local Similarity 58.34; Prd. No. 5.26-256;
Matches 4405; Conservative 0; Mismatches 2869; Indels 282; Gaps 19;

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 Db 134 GCAATTGAGGTAGTACAGACAGGCTGCTCAATGACATGACATGCTGCTGAGCTT 293
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 Oy 2884 tatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 2943
 Db 314 CTTGCTGATGTCACAGAACCCGACCCGATGATGATATGCGACTATGCGCGAAA 373
 Oy 2944 cctcgag 3003
 Db 374 AGCTCGAGGATTAAGAACAGAGACTTGCATGACAGATTAAGATCTACCGAGCT 403
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 Db 434 TGAAGCGAGTGTGTAACACAGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 493
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 Oy 3124 caacagaggtggaagaggtgcagagagagagagagagagagagagagagagagag 3183
 Db 551 TGCATGAGCTTGAAGAGAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 610
 Oy 3184 tatgttgcgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3243
 Db 611 CATGTTCTGGCTATGCGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 670
 Oy 3244 aggtgag 3303
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 Oy 3364 aggtgag 3423
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 Db 851 GTTCATCTGATGAGAGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 910
 Oy 3483 aggtgag 3543
 Db 911 AGCTGCTGTATGAGAGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 970
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 Oy 3604 ag 3663
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 Oy 3664 tggctctatcag 3723
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 Oy 3724 cag 3783
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 Db 1391 CCAGCTCTTTTAAAGCTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1450
 Oy 4024 agtcag 4083
 Db 1451 CTGAGGAGCAATTAAGAACTGGCATTCGACACAGAGAGAGAGAGAGAGAG 1510
 Oy 4084 tctgagcgtc-----gtcagcagagagagagagagagagagagagag 4137
 Db 1511 CTGCGAGAGATTAAGTCAATGAGCGAGAGCTGCTTTGAGCATCTGAGAGAGCAG 1570
 Oy 4138 agtcag 1630
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 Db 1931 ATGAG 1990
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[illegible]

[illegible]

Search completed: February 9, 2000, 05:39:30
Job time: 2795 sec

GenCore version 4.5
 Copyright (c) 1991 - 1998 CompuGen Ltd.
 OW nucleic - nucleic search, using sw model
 Run on: February 9, 2000, 07:45:53 Search time 9215.41 Seconds
 -5119.613 Million cell updates/sec

US-09-190-246-1
 Title: 15338
 Perfect score: 15338
 Sequence: 1 Cctccgcttgcgtatgc.....taccagagccttccttc 15338
 Scoring table: IDENTITY_NUC
 Searched: 821193 seqs, -1518192014 residues
 Database: GenEmbl.*
 Word size: 0

Number of hits that pass the threshold : 1642386

1: gb_hum1.*
 2: gb_hum1.*
 3: gb_hum1.*
 4: gb_hum1.*
 5: gb_ov.*
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 47: gb_ov.*
 48: gb_ov.*
 49: gb_ov.*

50. gb_p13.*

Pred. No. is the number of results predicted by chance to have a
 sum of equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	De	ID	Description
1	7399.2	47.6	11517	5	A18788	-----	Complete hu
2	7399.2	47.6	11517	5	A18788	-----	Complete hu
3	7399.2	47.6	11517	5	A18788	-----	Complete hu
4	7399.2	47.6	11517	5	A18788	-----	Complete hu
5	7399.2	47.6	11517	5	A18788	-----	Complete hu
6	7399.2	47.6	11517	5	A18788	-----	Complete hu
7	7399.2	47.6	11517	5	A18788	-----	Complete hu
8	7399.2	47.6	11517	5	A18788	-----	Complete hu
9	7399.2	47.6	11517	5	A18788	-----	Complete hu
10	7399.2	47.6	11517	5	A18788	-----	Complete hu
11	7399.2	47.6	11517	5	A18788	-----	Complete hu
12	7399.2	47.6	11517	5	A18788	-----	Complete hu
13	7399.2	47.6	11517	5	A18788	-----	Complete hu
14	7399.2	47.6	11517	5	A18788	-----	Complete hu
15	7399.2	47.6	11517	5	A18788	-----	Complete hu
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23	7399.2	47.6	11517	5	A18788	-----	Complete hu
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36	7399.2	47.6	11517	5	A18788	-----	Complete hu
37	7399.2	47.6	11517	5	A18788	-----	Complete hu
38	7399.2	47.6	11517	5	A18788	-----	Complete hu
39	7399.2	47.6	11517	5	A18788	-----	Complete hu
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44	7399.2	47.6	11517	5	A18788	-----	Complete hu
45	7399.2	47.6	11517	5	A18788	-----	Complete hu
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47	7399.2	47.6	11517	5	A18788	-----	Complete hu
48	7399.2	47.6	11517	5	A18788	-----	Complete hu
49	7399.2	47.6	11517	5	A18788	-----	Complete hu

ALIGNMENTS

RESULT 1
 LOCUS A18788 11517 bp
 DEFINITION complete nucleotide sequence of PSP6-STV4 RNA transcript.
 ACCESSION A18788
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM Homo sapiens.
 REFERENCE 1 (bases 1 to 11517)
 AUTHORS

06-MAY-1994

[illegible]

[illegible]

[illegible][illegible]

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ΑΠΤΗΘΕΣ

Lancioti, R.S., Ludwig, M.L., Rwanuma, E.B., Lutwama, J.J., Kram, T.M., Karabatsos, N., Cropp, B.C. and Miller, B.R.
Direct Submission
Submitted (21-JUL-1998) Division of Vector-Borne Diseases, Centers for Disease Control and Prevention, Rampart Rd., Fort Collins, CO

TITLE

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[illegible]

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